

# Package ‘wig’

May 8, 2026

**Type** Package

**Title** Import WIG Data into R in Long Format

**Version** 0.1.0

**Description** Import WIG data into R in long format.

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**URL** <https://github.com/ramiromagno/wig>

**BugReports** <https://github.com/ramiromagno/wig/issues>

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**Imports** dplyr, magrittr, stringr, tibble

**Suggests** spelling

**Language** en-US

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-10-04 08:20:02 UTC

## Contents

import_wig . . . . .	2
<b>Index</b>	<b>3</b>

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import_wig	<i>Imports a WIG file</i>
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### Description

import\_wig reads a **WIG (wiggle)** file and expands the data into long format, i.e., the each observation in the returned tibble pertains the position of one single base.

### Usage

```
import_wig(file_path, n = -1L)
```

### Arguments

file_path	A path to a WIG file.
n	The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.

### Value

A tibble of three variables: chr, chromosome; pos, genomic position; and val, value. Chromosome positions are 1-relative, i.e. the first base is 1, as specified in WIG files.

### Examples

```
# Import a WIG file
wig_file <- system.file(
  "extdata",
  file = 'hg19-pik3ca.wig',
  package = "wig",
  mustWork = TRUE)

import_wig(wig_file)
```

# Index

`import_wig`, 2